SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT:
 - (A) NAME: Bioteknologisk Institut
 - (B) STREET: Anker Engelunds Vej 1
 - (C) CITY: Lyngby
 - (D) COUNTRY: Denmark
 - (E) POSTAL CODE (ZIP): 2800
 - (ii) TITLE OF INVENTION: Recombinant Hexose Oxidase, a Method of Producing Same and Use of Such Enzyme
 - (iii) NUMBER OF SEQUENCES: 34
 - (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Tyr Glu Pro Tyr Gly Gly Val Pro 1 5

- (2) INFORMATION FOR SEQ ID NO: 2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ala Ile Ile Asn Val Thr Gly Leu Val Glu Ser Gly Tyr Asp Xaa Xaa 1 5 10 15

Xaa Gly Tyr Xaa Val Ser Ser

1

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Asp Leu Pro Met Ser Pro Arg Gly Val Ile Ala Ser Asn Leu Xaa Phe 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Asp Ser Glu Gly Asn Asp Gly Glu Leu Phe Xaa Ala His Thr
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Tyr Tyr Phe Lys

- (2) INFORMATION FOR SEQ ID NO: 6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Asp Pro Gly Tyr Ile Val Ile Asp Val Asn Ala Gly Thr Xaa Asp 10

- (2) INFORMATION FOR SEQ ID NO: 7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Leu Gln Tyr Gln Thr Tyr Trp Gln Glu Glu Asp

- (2) INFORMATION FOR SEQ ID NO: 8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Xaa Ile Arg Asp Phe Tyr Glu Glu Met

- (2) INFORMATION FOR SEQ ID NO: 9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Ala Ile Ile Asn Val Thr Gly Leu Val Glu Ser Gly Tyr Asp Xaa Xaa 10

Xaa Gly Tyr Xaa Val Ser Ser

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- (2) INFORMATION FOR SEQ ID NO: 10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B): TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Asp Leu Pro Met Ser Pro Arg Gly Val Ile Ala Ser Asn Leu Trp Phe 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Asp Ser Glu Gly Asn Asp Gly Glu Leu Phe Xaa Ala His Thr
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Tyr Tyr Phe Lys

- (2) INFORMATION FOR SEQ ID NO: 13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Asp Pro Gly Tyr Ile Val Ile Asp Val Asn Ala Gly Thr Pro Asp 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 14:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Leu Gln Tyr Gln Thr Tyr Trp Gln Glu Glu Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Xaa Ile Arg Asp Phe Tyr Glu Glu Met
1 5

- (2) INFORMATION FOR SEQ ID NO: 16:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (ix) FEATURE:
 - (A) NAME/KEY: modified base; N=inosine
 - (B) LOCATION: base pairs 3, 6 and 12
 - (C) IDENTIFICATION METHOD: commercially available
 - (D) OTHER INFORMATION
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

i...

	(A) LENGIN: 23 DASE DAILS	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid	
(i.s.)	FEATURE:	
(IX)	(A) NAME/KEY: modified base; N=inosine	
	(B) LOCATION: base pairs 6 and 12	
	(C) IDENTIFICATION METHOD: commercially available	
	(C) IDENTIFICATION METHOD: COMMETCIALLY AVAILABLE (D) OTHER INFORMATION	
	(D) OTHER INFORMATION	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 17:	
		.•
AACCANAR	RT TNGANGCDAT NAC	23
(2) 73770	DWARTON FOR CTO ID NO. 10.	
(2) INFO	RMATION FOR SEQ ID NO: 18:	
(;)	SEQUENCE CHARACTERISTICS:	
(± /	(A) LENGTH: 23 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(b) Torobodi. Timear	
(ii)	MOLECULE TYPE: other nucleic acid	
(ix)	FEATURE:	
(,	(A) NAME/KEY: modified base; N=inosine	
	(B) LOCATION: base pairs 6 and 15	
	(C) IDENTIFICATION METHOD: commercially available	
	(D) OTHER INFORMATION	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 18:	
GARGGNAA	YG AYGGNGARCT NTT	23
(2) TMEO	DARTON FOR CEO ID NO. 19.	
(2) INFO	RMATION FOR SEQ ID NO: 19:	
(;)	SEQUENCE CHARACTERISTICS:	
(1)	(A) LENGTH: 23 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(5) 10102001. 1111001	
(ii)	MOLECULE TYPE: other nucleic acid	
(ix)	FEATURE:	
,	(A) NAME/KEY: modified base; N=inosine	
	(B) LOCATION: base pairs 3 and 9	
	(C) IDENTIFICATION METHOD: commercially available	
	(D) OTHER INFORMATION	
	• • • • • • • • • • • • • • • • • • • •	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:	
AANAGYTCNC CRTCRTTNCC YTC	23
(2) INFORMATION FOR SEQ ID NO: 20:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: other nucleic acid	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:	
ATTGGGGCTC CTTCAAGACC TT	22
(2) INFORMATION FOR SEQ ID NO: 21:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: other nucleic acid	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:	
TGATGATTCC AAAGTTTC	18
(2) INFORMATION FOR SEQ ID NO: 22:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: other nucleic acid	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:	
TTGGAAGAAT ACGGTTGG	18
(2) INFORMATION FOR SEQ ID NO: 23:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: other nucleic acid

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(2)	INFO	RMATION FOR SEQ ID NO: 27:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: other nucleic acid	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 27:	
TGT	CGCAG	AC TGTACTTG	18
(2)	INFO	RMATION FOR SEQ ID NO: 28:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid . (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: other nucleic acid	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 28:	
GAG:	IGTAC	AC GACATAAA	18
(2)	INFO	RMATION FOR SEQ ID NO: 29:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 22 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii)	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
		(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
ATGG	(xi)	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear MOLECULE TYPE: other nucleic acid	22
	(xi)	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear MOLECULE TYPE: other nucleic acid SEQUENCE DESCRIPTION: SEQ ID NO: 29:	22
	(xi) GCTACT	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear MOLECULE TYPE: other nucleic acid SEQUENCE DESCRIPTION: SEQ ID NO: 29:	22

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:84..1721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

	(~ 1	, 35	QULIN	CL D	LJCK	1511	OIN.	JEQ .	ID N	O. 3	O .				
TGAATTCGTG GGTCGAAGAG CCCTTTGCCT CGTCTCTCTG GTACCGTGTA TGTCAAAGGT 6												r 60			
TCGCTTGCAC ACTGAACTTC ACG ATG GCT ACT CTT CCT CAG AAA GAC CCC Met Ala Thr Leu Pro Gln Lys Asp Pro 1 5														110	
						GTC Val									158
						AAG Lys									206
						TAT Tyr									254
						ATG Met								 	302
						TGC Cys 80									350
						GTC Val									398
						GTC Val									446
						GAC Asp									494
						GGT Gly									542
						GGC Gly 160									590
						GTC Val									638

GTC CAC AAA GAT TCC GAA GGC AAC GAC GGG GAC CTC TTT TGG GGA CAC Val His Lys Asp Ser Glu Gly Asn Asp Gly Glu Leu Phe Trp Ala His 190 ACA GGT GGC GGT GGC GGA AAC TTT GGA ATC ATC ACC AAA TAC TAC TTC Thr Gly Gly Gly Gly Gly Asn Phe Gly Ile Ile Thr Lys Tyr Tyr Phe 205 AAG GAT TTG CCC ATG TCT CCA CGG GGC GTC ATC GCA TCA AAT TTA CAC Lys Asp Leu Pro Met Ser Pro Arg Gly Val Ile Ala Ser Asn Leu His 225 TTC AGC TGG GAC GGT TTC ACA AGA GAG AGT GCC TTG CAG GAT TTG TTG ACA Phe Ser Trp Asp Gly Phe Thr Arg Asp Ala Leu Gln Asp Leu Leu Thr 235 AAG TAC TTC AAA CTT GCC AGA TGT GAT TGG AAG AAT ACG GTT GGC AAG Lys Tyr Phe Lys Leu Ala Arg Cys Asp Trp Lys Asn Thr Val Gly Lys 250 TTT CAA ATC TTC CAT CAG GCA GGG GAA GAG GAT GT GT ATC TTG TAT Phe Gln Ile Phe His Gln Ala Ala Glu Glu Phe Val Met Tyr Leu Tyr 270 ACA TCC TAC TCG AAC GAC GCC GAG CGC GAA GTT GCC CAA GAC CGT CAC Thr Ser Tyr Ser Asn Asp Ala Glu Arg Glu Val Ala Gln Asp Arg His 285 TAT CAT TTG GAG GCT GAC ATA GAA CAG ATC TAC AAA ACA TGC GAG CCC Tyr His Leu Glu Ala Asp Ile Glu Gln Ile Tyr Lys Thr Cys Glu Pro 300 ACC AAA GCG CTT GGC GGG GGA GTG GGG GGG CGC GTT CCC GTG CGG TAT Lys Ala Leu Gly Gly His Ala Gly Trp Ala Pro Phe Pro Val Arg 315 ACG CGC AAA GAG CAC ACA TCC AAG ACC GT TAC TAC TAC GAG ACG Pro Arg Lys Arg His Thr Ser Lys Thr Ser Tyr Met His Asp Glu Thr 330 ACG ATG TAC CCC TTC TAC GCG CTC ACT GAG ACG ATC AAC ACG ATC TAC AAA GCG CTT GCC GGG CTC ACT GAG ACG TAC Thr Lys Ala Leu Gly Gly His Ala Gly Trp Ala Pro Phe Pro Val Arg 315 ACG GCG AAA GCG CCC TCC TCC ACT GAG ACG ATC AAC ACC ACA TCC TAC TAC ACA ACA TCC AAG ACC TAC AAA ACA TCC CAG GCG CCG AAA GCG CCC TTC TAC GCG CTC ACT GAG ACC ATC Thr Lys Ala Leu Gly Cly His Ala Gly Trp Ala Pro Phe Pro Val Arg 315 ACG GCG CAG GCC ACA TCC ACG GCG GCC TC ACT GAG ACC ATC ACG GCG CTC ACT GCG GGC CTC ACT GAG ACC ACC ACA TCC CCC TTC TAC GCG CTC ACT GAG ACC ATC AAC GCC TCC GGG Met Asp Tyr Po Phe Tyr Ala Leu Thr Glu Thr Glu Val Pro 360 ACG GC TTG ACT AGT CCC GAA ATC AAG ACT TAC CAG GTG GTC CCG Pro Asp Phe Gln Ile Asp Val Ile Trp Lys Tyr												-						
Thr Gly Gly Gly Gly Asn Phe Gly Ile Ile Thr Lys Tyr Tyr Phe 210 AAG GAT TTG CCC ATG TCT CCA CGG GGC GTC ATC GCA TCA AAT TTA CAC Lys Asp Leu Pro Met Ser Pro Arg Gly Val Ile Ala Ser Asn Leu His 220 TTC AGC TGG GAC GGT TTC ACG AGA GAT GCC TTG CAG GAT TTG TTG ACA 830 Phe Ser Trp Asp Gly Phe Thr Arg Asp Ala Leu Gln Asp Leu Leu Thr 235 AAG TAC TTC AAA CTT GCC AGA TGT GAT TGG AAG AAT ACG GTT GGC AAG Lys Tyr Phe Lys Leu Ala Arg Cys Asp Trp Lys Asn Thr Val Gly Lys 250 TTC CAA ATC TTC CAT CAG GCA GCG GAA GAT GTU GTU ATG TAT TYR CAG ATC TAC AATC TTC CAT CAG GCA GCG GAA GAT TTG TTG TAT Phe Gln Ile Phe His Gln Ala Ala Glu Glu Phe Val Met Tyr Leu Tyr 270 ACA TCC TAC TCG AAC GAC GCC GAG CGC GAA GTT GCC CAA GAC CGT CAC Thr Ser Tyr Ser Asn Asp Ala Glu Arg Glu Val Ala Gln Asp Arg His 295 TAT CAT TTG GAG GCT GAC ATA GAA CAG ATC TAC AAA ACA TGC GAG CCC TYr His Leu Glu Ala Asp Ile Glu Gln Ile Tyr Lys Thr Cys Glu Pro 300 ACC AAA GCC CTT GGC GGG CAT GCT GGG TGG CGC CCT TC CCC GTG CGG Thr Lys Ala Leu Gly Gly His Ala Gly Trp Ala Pro Phe Pro Val Arg 315 ACC AAA GCG CTT GGC GGG CAT GCT GGG TGG CGC CCT TC CCC GTG CGG Thr Lys Ala Leu Gly Gly His Ala Gly Trp Ala Pro Phe Pro Val Arg 315 CCG CGC AAG AGG CAC ACA TCC AAG ACG TCG TAT ATG CAT GAC GAG ACG Thr ATG ATG Lys Arg His Thr Ser Lys Thr Ser Tyr Met His Asp Gly Ser Gly 355 ATG GAC TAC CCC TTC TAC GCG CTC ACT GAG ACG ATC AAT ATG GAC GAC TTC CAG GAG ACG TTC ATG AAT ATG CAT GAC GAG ACG TTC ATG GAC ATG ATC ATC ATG AAT ATG CAT GAC GAG ACG TTC ATG GAC ATG ATC ATG ATG ATG ATG ATT TTC ATG GAC ATT TTC AATH ATG CAT TAC AAT ATG CAT GAC GAT TTC TAC GAT TTC CAG GAT TTC TAC GAT TTC CAG GAT TTC TAC GAC GAT TTC TAC GAT	•					Ser					Gly					Ala	His	686
Lys Asp Leu Pro Met Ser Pro Arg Gly Val Ile Ala Ser Asn Leu His 220 TTC AGC TGG GAC GGT TTC ACG AGA GAG GAT GCC TTG CAG GAT TTG TTG ACA 240 Phe Ser Trp Asp Gly Phe Thr Arg Asp Ala Leu Gln Asp Leu Leu Thr 235 AAG TAC TTC AAA CTT GCC AGA TGT GAT TGG AAG AAT ACG GTT GGC AAG 240 AAG TAC TTC AAA CTT GCC AGA TGT GAT TGG AAG AAT ACG GTT GGC AAG 255 TTT CAA ATC TTC CAT CAG GCA GCG GAA GAG TTT GTC ATG TAC TTG TAT 270 Phe Gln Ile Phe His Gln Ala Ala Glu Glu Phe Val Met Tyr Leu Tyr 270 ACA TCC TAC TCG AAC GAC GCC GAG CGC GAA GTT GCC CAA GAC CGT CAC 374 Thr Ser Tyr Ser Asn Asp Ala Glu Arg Glu Val Ala Gln Asp Arg His 295 TAT CAT TTG GAG GCT GAC ATA GAA CAG ATC TAC AAA ACA TCC GAG CCC Tyr His Leu Glu Ala Asp Ile Glu Gln Ile Tyr Lys Thr Cys Glu Pro 300 ACC AAA GCG CTT GGC GGG CAT GCT GGG TGG CCC CTT CCC GTG CGG Thr Lys Ala Leu Gly Gly His Ala Gly Trp Ala Pro Phe Pro Val Arg 315 CCG CGC AAG AGG CAC ACA TCC AAG ACG TC GAT ATG CAT GAC GAG ACG TTC Tyr Ala Leu Gly Gly His Ala Leu Thr Glu Thr 340 ATG GAC TAC CCC TTC TAC GCG CTC ACT GAG ACG ATC AAC AGC GCC GAG CCC Thr Lys Arg His Thr Ser Lys Thr Ser Tyr Met His Asp Glu Thr 330 ATG GAC TAC CCC TTC TAC GCG CTC ACT GAG ACG ATC AAC AGC GCC GGG TCC GGG Met Asp Tyr Pro Phe Tyr Ala Leu Thr Glu Thr Ile Asn Gly Ser Gly 355 CCG AAT CAG CGC GGC AAG TAC AAG TCT GCG TAC ATC AAG ACG TCC GGG TCC GGG Met Asp Tyr Pro Phe Tyr Ala Leu Thr Glu Thr Ile Asn Gly Ser Gly 355 CCG GAT CAG CGC GGC AAG TAC AAG TCT GCG TAC ATC ATC AAG AGT TCC AGG GAT TCC AGG GAT CAC GGC TCC GGG TTC CCC GGG ATC AAC GGC TCC GGG TTC CCC GTG GAT TCC CAG GTG GAC ATC ASP Phe Gln Tle Asp Val Tyr Lys Ser Ala Tyr Met Ile Lys Asp Phe 375 CCG GAT TCC CAG ATC GAC GTG ATC TGG AAA TAC CTT ACG GAG GTC CCG Pro Asp Phe Gln Ile Asp Val Ile Trp Lys Tyr Let Thr Glu Val Pro 380 GAC GGC TTG ACT ACT GCC GAA ATG AAG GAT GCC TTA CTC CAG GTG GAC ASP GAC GCC CTG AATC AATC ACT GCC GAC GTG GAC ASP ASP ALA Leu Leu Gly Leu Thr Ser Ala Glu Met Lys Asp Ala Leu Leu Gln Val Asp					Gly					Gly					Tyr			734
Phe Ser Trp Asp Gly Phe Thr Arg Asp Ala Leu Gln Asp Leu Leu Thr 245 AAG TAC TTC AAA CTT GCC AGA TGT GAT TGG AAG AAT ACG GTT GGC AAG 878 Lys Tyr Phe Lys Leu Ala Arg Cys Asp Trp Lys Asn Thr Val Gly Lys 250 TTT CAA ATC TTC CAT CAG GCA GCG GAA GAG TTT GTC ATG TAC TTG TAT Phe Gln Ile Phe His Gln Ala Ala Glu Glu Phe Val Met Tyr Leu Tyr 270 ACA TCC TAC TCG AAC GAC GCC GAG CGC GAA GTT GCC CAA GAC CGT CAC PAC Thr Ser Tyr Ser Asn Asp Ala Glu Arg Glu Val Ala Gln Asp Arg His 285 TAT CAT TTG GAG GCT GAC ATA GAA CAG ATC TAC AAA ACA TGC GAG CCC Tyr His Leu Glu Ala Asp Ile Glu Gln Ile Tyr Lys Glu Pro 300 ACC AAA GCG CTT GGC GGG CAT GCT GGG TGG GCG CCG TTC CCC GTG CGG TYR Lys Ala Leu Gly Gly His Ala Gly Trp Ala Pro Phe Pro Val Arg 315 CCG CGC AAG AGG CAC ACA TCC AAG ACG TCG TAT ATG CAT GAC GAG ACG Thr ATG ARG ACG ACG ACG ACG ACG ACG ACG ACG ACG AC				Leu					Arg			-		Ser				782
Lys Tyr Phe Lys Leu Ala Arg Cys Asp Trp Lys Asn Thr Val Gly Lys 265 TTT CAA ATC TTC CAT CAG GCA GCG GAA GAG TTT GTC ATG TAC TTG TAT Phe Gln Ile Phe His Gln Ala Ala Glu Glu Phe Val Met Tyr Leu Tyr 270 ACA TCC TAC TCG AAC GAC GCC GAG CGC GAA GTT GCC CAA GAC CGT CAC Phe Gln Tr Ser Asn Asp Ala Glu Arg Glu Val Ala Gln Asp Arg His 295 TAT CAT TTG GAG GCT GAC ATA GAA CAG ATC TAC AAA ACA TGC GAG CCC TYr His Leu Glu Ala Asp Ile Glu Gln Ile Tyr Lys Thr Cys Glu Pro 300 ACC AAA GCG CTT GGC GGG CAT GCT GGG TGG GCG CCG TTC CCC GTG CGG 1070 Thr Lys Ala Leu Gly Gly His Ala Gly Trp Ala Pro Phe Pro Val Arg 315 CCG CGC AAG AGG CAC ACA TCC AAG ACG TCG TAT ATG CAT GAC GAG ACG Thr Ser Lys Thr Ser Lys Thr Ser Tyr Met His Asp Glu Thr 330 ATG GAC TAC CCC TTC TAC GCG CTC ACT GAG ACG ATC AAC GGC TCC GGG Met Asp Tyr Pro Phe Tyr Ala Leu Thr Glu Thr Ile Asn Gly Ser Gly 355 CCG AAT CAG CGC GGC AAG TAC AAG TCT GCG TAC ATG ATC AAC GGC TCC GGG TGC CCG AAT CAC GAG ACG TTC CCC GTG CGG AAT CAC GAC GAG ACG TCT GAT ATG CAT CAC GAG ACG TTC CCC GTG CGG Met Asp Tyr Pro Phe Tyr Ala Leu Thr Glu Thr Ile Asn Gly Ser Gly 350 CCG AAT CAG CGC GGC AAG TAC AAG TCT GCG TAC ATG ATC AAC GGC TCC GGG T166 Met Asp Tyr Pro Phe Tyr Ala Leu Thr GC ATG ATC AAC GAC TCC GGG T166 CCG GAT TCC CAC ACA TCC AAG TCT GCG TAC ATG ATC AAC GAC TCC GGC TCC GGG TAC ATG ATG ATC AAC GAC TCC ASP ASP Phe Gln Arg Gly Lys Tyr Lys Ser Ala Tyr Met Ile Lys Asp Phe 365 CCC GAT TCC CAC ACA TCC AAC TCC AAC TCG AAC TCC TAC ATG ATC AAC GAC TCC CCC PTO Asp Phe Gln Ile Asp Val Ile Trp Lys Tyr Leu Thr Glu Val Pro 380 GAC GGC TTG ACT ACT ACT GCC GAA ATG AAG GAT GCC TTA CTC CAC GTG GAC 1310 ASP Gly Leu Thr Ser Ala Glu Met Lys Asp Ala Leu Leu Gln Val Asp			Ser					Thr					Gln					830
Phe Gln Ile Phe His Gln Ala Ala Glu Glu Phe Val Met Tyr Leu Tyr 280 ACA TCC TAC TCG AAC GAC GCC GAG CGC GAA GTT GCC CAA GAC CGT CAC 774 Thr Ser Tyr Ser Asn Asp Ala Glu Arg Glu Val Ala Gln Asp Arg His 285 TAT CAT TTG GAG GCT GAC ATA GAA CAG ATC TAC AAA ACA TGC GAG CCC 774 This Leu Glu Ala Asp Ile Glu Gln Ile Tyr Lys Thr Cys Glu Pro 300 ACC AAA GCG CTT GGC GGG CAT GCT GGG TGG GCG CCG TTC CCC GTG CGG 1070 Thr Lys Ala Leu Gly Gly His Ala Gly Trp Ala Pro Phe Pro Val Arg 315 CCG CGC AAG AGG CAC ACA TCC AAG ACG TCG TAT ATG CAT GAC GAG ACG ATG ATG AAG ACG ATG AAG ACG ACG ATG AAG ACG ACG ATG AAG ACG ACG ATG AAG ACG ACG ACG ACG ACG ACG ACG ACG AC		Lys	Tyr				Ala					Lys					Lys	
Thr Ser Tyr Ser Asn Asp Ala Glu Arg Glu Val Ala Gln Asp Arg His 285 TAT CAT TTG GAG GCT GAC ATA GAA CAG ATC TAC AAA ACA TGC GAG CCC Tyr His Leu Glu Ala Asp Ile Glu Gln Ile Tyr Lys Thr Cys Glu Pro 300 ACC AAA GCG CTT GGC GGG CAT GCT GGG TGG GCG CCG TTC CCC GTG CGG 1070 Thr Lys Ala Leu Gly Gly His Ala Gly Trp Ala Pro Phe Pro Val Arg 315 CCG CGC AAG AGG CAC ACA TCC AAG ACG TCG TAT ATG CAT GAC GAG ACG 1118 Pro Arg Lys Arg His Thr Ser Lys Thr Ser Tyr Met His Asp Glu Thr 330 ATG GAC TAC CCC TTC TAC GCG CTC ACT GAG ACG ATC AAC GGC TCC GGG Met Asp Tyr Pro Phe Tyr Ala Leu Thr Glu Thr Ile Asn Gly Ser Gly 350 CCG AAT CAG CGC GGC AAG TAC AAG TCT GCG TAC ATG ATC AAG GAT TTC 1214 Pro Asn Gln Arg Gly Lys Tyr Lys Ser Ala Tyr Met Ile Lys Asp Phe 365 CCG GAT TTC CAG ATC GAC GTG ATC TGG AAA TAC CTT ACG GAG GTC CCG Pro Asp Phe Gln Ile Asp Val Ile Trp Lys Tyr Leu Thr Glu Val Pro 380 Gly Leu Thr Ser Ala Glu Met Lys Asp Ala Leu Leu Gln Val Asp						His					Glu					Leu		926
Tyr His Leu Glu Ala Asp Ile Glu Gln Ile Tyr Lys Thr Cys Glu Pro 300 305 305 310 310 310 310 310 310 310 310 310 310					Ser					Arg					Asp			974
Thr Lys Ala Leu Gly Gly His Ala Gly Trp Ala Pro Phe Pro Val Arg 315 CCG CGC AAG AGG CAC ACA TCC AAG ACG TCG TAT ATG CAT GAC GAG ACG Pro Arg Lys Arg His Thr Ser Lys Thr Ser Tyr Met His Asp Glu Thr 330 ATG GAC TAC CCC TTC TAC GCG CTC ACT GAG ACG ATC AAC GGC TCC GGG Met Asp Tyr Pro Phe Tyr Ala Leu Thr Glu Thr Ile Asn Gly Ser Gly 350 CCG AAT CAG CGC GGC AAG TAC AAG TCT GCG TAC ATG ATC AAG GAT TTC Pro Asn Gln Arg Gly Lys Tyr Lys Ser Ala Tyr Met Ile Lys Asp Phe 365 CCG GAT TTC CAG ATC GAC GTG ATC TGG AAA TAC CTT ACG GAG GTC CCG Pro Asp Phe Gln Ile Asp Val Ile Trp Lys Tyr Leu Thr Glu Val Pro 380 GAC GGC TTG ACT AGT GCC GAA ATG AAG GAT GCC TTA CTC CAG GTG GAC Asp Gly Leu Thr Ser Ala Glu Met Lys Asp Ala Leu Leu Gln Val Asp				Leu					Glu					Thr				1022
Pro Arg Lys Arg His Thr Ser Lys Thr Ser Tyr Met His Asp Glu Thr 330 335 335 340 345 ATG GAC TAC CCC TTC TAC GCG CTC ACT GAG ACG ATC AAC GGC TCC GGG 1166 Met Asp Tyr Pro Phe Tyr Ala Leu Thr Glu Thr Ile Asn Gly Ser Gly 350 355 360 CCG AAT CAG CGC GGC AAG TAC AAG TCT GCG TAC ATG ATC AAG GAT TTC Pro Asn Gln Arg Gly Lys Tyr Lys Ser Ala Tyr Met Ile Lys Asp Phe 365 370 375 CCG GAT TTC CAG ATC GAC GTG ATC TGG AAA TAC CTT ACG GAG GTC CCG Pro Asp Phe Gln Ile Asp Val Ile Trp Lys Tyr Leu Thr Glu Val Pro 380 385 390 GAC GGC TTG ACT AGT GCC GAA ATG AAG GAT GCC TTA CTC CAG GTG GAC 1310 Asp Gly Leu Thr Ser Ala Glu Met Lys Asp Ala Leu Leu Gln Val Asp			Lys					His					Pro					1070
Met Asp Tyr Pro Phe Tyr Ala Leu Thr Glu Thr Ile Asn Gly Ser Gly 350 CCG AAT CAG CGC GGC AAG TAC AAG TCT GCG TAC ATG ATC AAG GAT TTC Pro Asn Gln Arg Gly Lys Tyr Lys Ser Ala Tyr Met Ile Lys Asp Phe 365 CCG GAT TTC CAG ATC GAC GTG ATC TGG AAA TAC CTT ACG GAG GTC CCG Pro Asp Phe Gln Ile Asp Val Ile Trp Lys Tyr Leu Thr Glu Val Pro 380 GAC GGC TTG ACT AGT GCC GAA ATG AAG GAT GCC TTA CTC CAG GTG GAC 1310 Asp Gly Leu Thr Ser Ala Glu Met Lys Asp Ala Leu Leu Gln Val Asp		Pro	Arg			His	Thr				Ser	Tyr					Thr	1118
Pro Asn Gln Arg Gly Lys Tyr Lys Ser Ala Tyr Met Ile Lys Asp Phe 365 370 375 CCG GAT TTC CAG ATC GAC GTG ATC TGG AAA TAC CTT ACG GAG GTC CCG 1262 Pro Asp Phe Gln Ile Asp Val Ile Trp Lys Tyr Leu Thr Glu Val Pro 380 385 390 GAC GGC TTG ACT AGT GCC GAA ATG AAG GAT GCC TTA CTC CAG GTG GAC 1310 Asp Gly Leu Thr Ser Ala Glu Met Lys Asp Ala Leu Leu Gln Val Asp						Phe					Glu					Ser		1166
Pro Asp Phe Gln Ile Asp Val Ile Trp Lys Tyr Leu Thr Glu Val Pro 380 385 390 GAC GGC TTG ACT AGT GCC GAA ATG AAG GAT GCC TTA CTC CAG GTG GAC 1310 Asp Gly Leu Thr Ser Ala Glu Met Lys Asp Ala Leu Leu Gln Val Asp					Arg					Ser					Lys			1214
Asp Gly Leu Thr Ser Ala Glu Met Lys Asp Ala Leu Leu Gln Val Asp				Phe					Ile					Thr				1262
			Gly					Glu					Leu					1310

				ATT Ile 415										1358
				ATC Ile										1406
		 _	_	GCA Ala	 _		_			_				1454
				CCG Pro										1502
				GGT Gly										1550
		 	_	AAC Asn 495	 Lys	_							_	1598
-				AAC Asn										1646
	_	 _	_	ATC Ile	-	-				_		-		1694
				AAG Lys			TAGT	ragg1	CA (CAATT	ragt(CA .		1741

TCGACTGAAG TGCAGCACTT GTCGGATACG GCGTGATGGT TGCTTTTTAT AAACTTGGTA 1801

- (2) INFORMATION FOR SEQ ID NO: 31:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 546 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met Ala Thr Leu Pro Gln Lys Asp Pro Gly Tyr Ile Val Ile Asp Val 1 5 10 15

Asn Ala Gly Thr Ala Asp Lys Pro Asp Pro Arg Leu Pro Ser Met Lys
20 25 30

Gln Gly Phe Asn Arg Arg Trp Ile Gly Thr Asn Ile Asp Phe Val Tyr

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Val Val Tyr Thr Pro Gln Gly Ala Cys Thr Ala Leu Asp Arg Ala Met Glu Lys Cys Ser Pro Gly Thr Val Arg Ile Val Ser Gly Gly His Cys Tyr Glu Asp Phe Val Phe Asp Glu Cys Val Lys Ala Ile Ile Asn Val Thr Gly Leu Val Glu Ser Gly Tyr Asp Asp Asp Arg Gly Tyr Phe Val 105 Ser Ser Gly Asp Thr Asn Trp Gly Ser Phe Lys Thr Leu Phe Arg Asp 120 His Gly Arg Val Leu Pro Gly Gly Ser Cys Tyr Ser Val Gly Leu Gly Gly His Ile Val Gly Gly Gly Asp Gly Ile Leu Ala Arg Leu His Gly Leu Pro Val Asp Trp Leu Ser Gly Val Glu Val Val Val Lys Pro Val Leu Thr Glu Asp Ser Val Leu Lys Tyr Val His Lys Asp Ser Glu Gly 180 Asn Asp Gly Glu Leu Phe Trp Ala His Thr Gly Gly Gly Gly Asn 200 Phe Gly Ile Ile Thr Lys Tyr Tyr Phe Lys Asp Leu Pro Met Ser Pro 210 215 220 Arg Gly Val Ile Ala Ser Asn Leu His Phe Ser Trp Asp Gly Phe Thr Arg Asp Ala Leu Gln Asp Leu Leu Thr Lys Tyr Phe Lys Leu Ala Arg 250 Cys Asp Trp Lys Asn Thr Val Gly Lys Phe Gln Ile Phe His Gln Ala 260 Ala Glu Glu Phe Val Met Tyr Leu Tyr Thr Ser Tyr Ser Asn Asp Ala Glu Arg Glu Val Ala Gln Asp Arg His Tyr His Leu Glu Ala Asp Ile 290 Glu Gln Ile Tyr Lys Thr Cys Glu Pro Thr Lys Ala Leu Gly Gly His Ala Gly Trp Ala Pro Phe Pro Val Arg Pro Arg Lys Arg His Thr Ser 330 Lys Thr Ser Tyr Met His Asp Glu Thr Met Asp Tyr Pro Phe Tyr Ala 345

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Leu Thr Glu Thr Ile Asn Gly Ser Gly Pro Asn Gln Arg Gly Lys Tyr 355 360 365

Lys Ser Ala Tyr Met Ile Lys Asp Phe Pro Asp Phe Gln Ile Asp Val 370 : 375 380

Ile Trp Lys Tyr Leu Thr Glu Val Pro Asp Gly Leu Thr Ser Ala Glu 385 390 395 400

Met Lys Asp Ala Leu Leu Gln Val Asp Met Phe Gly Gly Glu Ile His
405 410 415

Lys Val Val Trp Asp Ala Thr Ala Val Ala Gln Arg Glu Tyr Ile Ile 420 425 430

-Lys Leu Gln Tyr Gln Thr Tyr Trp Gln Glu Glu Asp Lys Asp Ala Val 435 440 445

Asn Leu Lys Trp Ile Arg Asp Phe Tyr Glu Glu Met Tyr Glu Pro Tyr 450 455 . 460

Gly Gly Val Pro Asp Pro Asn Thr Gln Val Glu Ser Gly Lys Gly Val 465 470 475 480

Phe Glu Gly Cys Tyr Phe Asn Tyr Pro Asp Val Asp Leu Asn Asn Trp
485 490 495

Lys Asn Gly Lys Tyr Gly Ala Leu Glu Leu Tyr Phe Leu Gly Asn Leu 500 505 510

Asn Arg Leu Ile Lys Ala Lys Trp Leu Trp Asp Pro Asn Glu Ile Phe 515 520 525

Thr Asn Lys Gln Ser Ile Pro Thr Lys Pro Leu Lys Glu Pro Lys Gln 530 535 540

Thr Lys 545

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ACCAAGTTTA TAAAAAGCAA CCATCAC

33

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	2.0	
(2) I	NFORMATION FOR SEQ ID NO: 33:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B): TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(:	ii) MOLECULE TYPE: other nucleic acid	
()	xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:	
ATGAA	ITCGT GGGTCGAAGA GCCC	24
(2) II	NFORMATION FOR SEQ ID NO: 34:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
i)	ii) MOLECULE TYPE: other nucleic acid	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CAGGAATTCA TATGGCTACT CTTCCCCAGA AAG